

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: TSUJI, SHOJI
SANPEI, KAZUHIRO

(ii) TITLE OF INVENTION: cDNA FRAGMENT OF CAUSATIVE GENE OF
SPINOCEREBELLAR ATAXIA TYPE 2

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
(B) STREET: P.O. Box 747
(C) CITY: Falls Church
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MURPHY Jr., Gerald M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 0760-0248P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 205-8000
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 49..3987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TATCCGCACC TCCGCTCCCA CCCGGCGCCT CGGCGCGCCC GCCCTCCG ATG CGC TCA

57

Met Arg Ser

1

GCG GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC	105
Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg	
5 10 15	
TTC GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG	153
Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala	
20 25 30 35	
CGG CGG AGC GGG CGG GGC GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC	201
Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro	
40 45 50	
TCC GCC GCC CCT CCC CCG CCC GGC CCC GGC CCC CCT CCC TCC CGG CAG	249
Ser Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Pro Ser Arg Gln	
55 60 65	
AGC TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC	297
Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly	
70 75 80	
GGC GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG	345
Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Gly Leu Gly Gly	
85 90 95	
CCT CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC	393
Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly	
100 105 110 115	
GCC CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG	441
Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala	
120 125 130	
TCC CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT	489
Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala Pro Gly Cys	
135 140 145	
CCC CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG	537
Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu	
150 155 160	
AAG CCC CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CAA	585
Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln	
165 170 175	
CAG CAG CAG CAG CAG CAG CAG CAG CAG CAG CCG CCG CCC GCG GCT GCC AAT	633
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala Ala Ala Asn	
180 185 190 195	
GTC CGC AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCC GCG	681
Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala	
200 205 210	
CCT TCG CCG TCC TCG TCC TCG GTC TCC TCG TCC TCG GCC ACG GCT CCC	729
Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala Thr Ala Pro	
215 220 225	
TCC TCG GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC	777
Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly	

230	235	240	
AGA GGT CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe 245 250 255			825
GAT GGA ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val 260 265 270 275			873
GTT GGC TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu 280 285 290			921
GGA GTT TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala 295 300 305			969
GCA CAT GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys Arg Glu Glu 310 315 320			1017
ATA ATG GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln 325 330 335			1065
TTT AAA GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp 340 345 350 355			1113
TCT GCT ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu 360 365 370			1161
GAG CCC TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala 375 380 385			1209
TTG GAA AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA Leu Glu Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg 390 395 400			1257
TAT AAT GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA Tyr Asn Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu 405 410 415			1305
TCT TCG TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA Ser Ser Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu 420 425 430 435			1353
AAA CGG GAA GCA AGG GCA AAC CAG TTA GCA GAA GAA ATT GAG TCA AGT Lys Arg Glu Ala Arg Ala Asn Gln Leu Ala Glu Glu Ile Glu Ser Ser 440 445 450			1401
GCC CAG TAC AAA GCT CGA GTG GCC CTG GAA AAC GAT GAT AGG AGT GAG Ala Gln Tyr Lys Ala Arg Val Ala Leu Glu Asn Asp Asp Arg Ser Glu 455 460 465			1449
GAA GAA AAA TAC ACA GCA GTT CAG AGA AAT TCC AGT GAA CGT GAG GGG Glu Glu Lys Tyr Thr Ala Val Gln Arg Asn Ser Ser Glu Arg Glu Gly 470 475 480			1497

CAC AGC ATA AAC ACT AGG GAA AAT AAA TAT ATT CCT CCT GGA CAA AGA His Ser Ile Asn Thr Arg Glu Asn Lys Tyr Ile Pro Pro Gly Gln Arg 485 490 495	1545
AAT AGA GAA GTC ATA TCC TGG GGA AGT GGG AGA CAG AAT TCA CCG CGT Asn Arg Glu Val Ile Ser Trp Gly Ser Gly Arg Gln Asn Ser Pro Arg 500 505 510 515	1593
ATG GGC CAG CCT GGA TCG GGC TCC ATG CCA TCA AGA TCC ACT TCT CAC Met Gly Gln Pro Gly Ser Gly Ser Met Pro Ser Arg Ser Thr Ser His 520 525 530	1641
ACT TCA GAT TTC AAC CCG AAT TCT GGT TCA GAC CAA AGA GTA GTT AAT Thr Ser Asp Phe Asn Pro Asn Ser Gly Ser Asp Gln Arg Val Val Asn 535 540 545	1689
GGA GGT GTT CCC TGG CCA TCG CCT TGC CCA TCT CCT TCC TCT CGC CCA Gly Gly Val Pro Trp Pro Ser Pro Cys Pro Ser Pro Ser Ser Arg Pro 550 555 560	1737
CCT TCT CGC TAC CAG TCA GGT CCC AAC TCT CTT CCA CCT CGG GCA GCC Pro Ser Arg Tyr Gln Ser Gly Pro Asn Ser Leu Pro Pro Arg Ala Ala 565 570 575	1785
ACC CCT ACA CGG CCG CCC TCC AGG CCC CCC TCG CGG CCA TCC AGA CCC Thr Pro Thr Arg Pro Pro Ser Arg Pro Pro Ser Arg Pro Ser Arg Pro 580 585 590 595	1833
CCG TCT CAC CCC TCT GCT CAT GGT TCT CCA GCT CCT GTC TCT ACT ATG Pro Ser His Pro Ser Ala His Gly Ser Pro Ala Pro Val Ser Thr Met 600 605 610	1881
CCT AAA CGC ATG TCT TCA GAA GGG CCT CCA AGG ATG TCC CCA AAG GCC Pro Lys Arg Met Ser Ser Glu Gly Pro Pro Arg Met Ser Pro Lys Ala 615 620 625	1929
CAG CGA CAT CCT CGA AAT CAC AGA GTT TCT GCT GGG AGG GGT TCC ATA Gln Arg His Pro Arg Asn His Arg Val Ser Ala Gly Arg Gly Ser Ile 630 635 640	1977
TCC AGT GGC CTA GAA TTT GTA TCC CAC AAC CCA CCC AGT GAA GCA GCT Ser Ser Gly Leu Glu Phe Val Ser His Asn Pro Pro Ser Glu Ala Ala 645 650 655	2025
ACT CCT CCA GTA GCA AGG ACC AGT CCC TCG GGG GGA ACG TGG TCA TCA Thr Pro Pro Val Ala Arg Thr Ser Pro Ser Gly Gly Thr Trp Ser Ser 660 665 670 675	2073
GTG GTC AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG Val Val Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg 680 685 690	2121
TCT CCC AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT Ser Pro Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu 695 700 705	2169
GCT TCT CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro 710 715 720	2217

ATT CCA GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala 725 730 735	2265
GTT ACC CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg 740 745 750 755	2313
CAG AAC TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr 760 765 770	2361
TCA CCT AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val 775 780 785	2409
TCT GAA CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp 790 795 800	2457
TTT AGG TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu 805 810 815	2505
AAC AAA AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys 820 825 830 835	2553
ATT GAA CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Ser Asn 840 845 850	2601
TGT ACC AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser 855 860 865	2649
ATA CTT AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln 870 875 880	2697
GGG GTT CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys 885 890 895	2745
GAA GAG AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn 900 905 910 915	2793
CCC AAT GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro 920 925 930	2841
TCT ACT ACC CCA ACT TCA CCT CGG CCT CAA GCA CAA CCT AGC CCA TCT Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro Ser Pro Ser 935 940 945	2889
ATG GTG GGT CAT CAA CAG CCA ACT CCA GTT TAT ACT CAG CCT GTT TGT Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln Pro Val Cys 950 955 960	2937
TTT GCA CCA AAT ATG ATG TAT CCA GTC CCA GTG AGC CCA GGC GTG CAA	2985

Phe	Ala	Pro	Asn	Met	Met	Tyr	Pro	Val	Pro	Val	Ser	Pro	Gly	Val	Gln		
965						970					975						
CCT	TTA	TAC	CCA	ATA	CCT	ATG	ACG	CCC	ATG	CCA	GTG	AAT	CAA	GCC	AAG	3033	
Pro	Leu	Tyr	Pro	Ile	Pro	Met	Thr	Pro	Met	Pro	Val	Asn	Gln	Ala	Lys		
980					985					990					995		
ACA	TAT	AGA	GCA	GTA	CCA	AAT	ATG	CCC	CAA	CAG	CGG	CAA	GAC	CAG	CAT	3081	
Thr	Tyr	Arg	Ala	Val	Pro	Asn	Met	Pro	Gln	Gln	Arg	Gln	Asp	Gln	His		
				1000					1005					1010			
CAT	CAG	AGT	GCC	ATG	ATG	CAC	CCA	GCG	TCA	GCA	GCG	GGC	CCA	CCG	ATT	3129	
His	Gln	Ser	Ala	Met	Met	His	Pro	Ala	Ser	Ala	Ala	Gly	Pro	Pro	Ile		
			1015					1020					1025				
GCA	GCC	ACC	CCA	CCA	GCT	TAC	TCC	ACG	CAA	TAT	GTT	GCC	TAC	AGT	CCT	3177	
Ala	Ala	Thr	Pro	Pro	Ala	Tyr	Ser	Thr	Gln	Tyr	Val	Ala	Tyr	Ser	Pro		
			1030					1035					1040				
CAG	CAG	TTC	CCA	AAT	CAG	CCC	CTT	GTT	CAG	CAT	GTG	CCA	CAT	TAT	CAG	3225	
Gln	Gln	Phe	Pro	Asn	Gln	Pro	Leu	Val	Gln	His	Val	Pro	His	Tyr	Gln		
	1045					1050					1055						
TCT	CAG	CAT	CCT	CAT	GTC	TAT	AGT	CCT	GTA	ATA	CAG	GGT	AAT	GCT	AGA	3273	
Ser	Gln	His	Pro	His	Val	Tyr	Ser	Pro	Val	Ile	Gln	Gly	Asn	Ala	Arg		
1060					1065					1070					1075		
ATG	ATG	GCA	CCA	CCA	ACA	CAC	GCC	CAG	CCT	GGT	TTA	GTA	TCT	TCT	TCA	3321	
Met	Met	Ala	Pro	Pro	Thr	His	Ala	Gln	Pro	Gly	Leu	Val	Ser	Ser	Ser		
				1080					1085					1090			
GCA	ACT	CAG	TAC	GGG	GCT	CAT	GAG	CAG	ACG	CAT	GCG	ATG	TAT	GCA	TGT	3369	
Ala	Thr	Gln	Tyr	Gly	Ala	His	Glu	Gln	Thr	His	Ala	Met	Tyr	Ala	Cys		
			1095					1100					1105				
CCC	AAA	TTA	CCA	TAC	AAC	AAG	GAG	ACA	AGC	CCT	TCT	TTC	TAC	TTT	GCC	3417	
Pro	Lys	Leu	Pro	Tyr	Asn	Lys	Glu	Thr	Ser	Pro	Ser	Phe	Tyr	Phe	Ala		
		1110					1115						1120				
ATT	TCC	ACG	GGC	TCC	CTT	GCT	CAG	CAG	TAT	GCG	CAC	CCT	AAC	GCT	ACC	3465	
Ile	Ser	Thr	Gly	Ser	Leu	Ala	Gln	Gln	Tyr	Ala	His	Pro	Asn	Ala	Thr		
	1125					1130					1135						
CTG	CAC	CCA	CAT	ACT	CCA	CAC	CCT	CAG	CCT	TCA	GCT	ACC	CCC	ACT	GGA	3513	
Leu	His	Pro	His	Thr	Pro	His	Pro	Gln	Pro	Ser	Ala	Thr	Pro	Thr	Gly		
1140					1145					1150					1155		
CAG	CAG	CAA	AGC	CAA	CAT	GGT	GGA	AGT	CAT	CCT	GCA	CCC	AGT	CCT	GTT	3561	
Gln	Gln	Gln	Ser	Gln	His	Gly	Gly	Ser	His	Pro	Ala	Pro	Ser	Pro	Val		
				1160				1165						1170			
CAG	CAC	CAT	CAG	CAC	CAG	GCC	GCC	CAG	GCT	CTC	CAT	CTG	GCC	AGT	CCA	3609	
Gln	His	His	Gln	His	Gln	Ala	Ala	Gln	Ala	Leu	His	Leu	Ala	Ser	Pro		
				1175				1180					1185				
CAG	CAG	CAG	TCA	GCC	ATT	TAC	CAC	GCG	GGG	CTT	GCG	CCA	ACT	CCA	CCC	3657	
Gln	Gln	Gln	Ser	Ala	Ile	Tyr	His	Ala	Gly	Leu	Ala	Pro	Thr	Pro	Pro		
			1190				1195					1200					
TCC	ATG	ACA	CCT	GCC	TCC	AAC	ACG	CAG	TCG	CCA	CAG	AAT	AGT	TTC	CCA	3705	
Ser	Met	Thr	Pro	Ala	Ser	Asn	Thr	Gln	Ser	Pro	Gln	Asn	Ser	Phe	Pro		

1205	1210	1215	
GCA GCA CAA CAG ACT GTC TTT ACG ATC CAT CCT TCT CAC GTT CAG CCG			3753
Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His Val Gln Pro			
1220	1225	1230	1235
GCG TAT ACC AAC CCA CCC CAC ATG GCC CAC GTA CCT CAG GCT CAT GTA			3801
Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln Ala His Val			
1240	1245	1250	
CAG TCA GGA ATG GTT CCT TCT CAT CCA ACT GCC CAT GCG CCA ATG ATG			3849
Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala Pro Met Met			
1255	1260	1265	
CTA ATG ACG ACA CAG CCA CCC GGC GGT CCC CAG GCC GCC CTC GCT CAA			3897
Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala Leu Ala Gln			
1270	1275	1280	
AGT GCA CTA CAG CCC ATT CCA GTC TCG ACA ACA GCG CAT TTC CCC TAT			3945
Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His Phe Pro Tyr			
1285	1290	1295	
ATG ACG CAC CCT TCA GTA CAA GCC CAC CAC CAA CAG CAG TTG			3987
Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln Leu			
1300	1305	1310	
TAAGGCTGCC CTGGAGGAAC CGAAAGGCCA AATTCCTCC TCCCTTCTAC TGCTTCTACC			4047
AACTGGAAGC ACAGAAAAC TGAATTTTCAT TTATTTTGTT TTTAAAATAT ATATGTTGAT			4107
TTCTTGTAAC ATCCAATAGG AATGCTAACA GTTCACTTGC AGTGGAAGAT ACTTGGACCG			4167
AGTAGAGGCA TTTAGGAACT TGGGGGCTAT TCCATAATTC CATATGCTGT TTCAGAGTCC			4227
CGCAGGTACC CCAGCTCTGC TTGCCGAAAC TGGAAGTTAT TTATTTTTTA ATAACCCTTG			4287
AAAGTCATGA ACACATCAGC TAGCAAAAAGA AGTAACAAGA GTGATTCTTG CTGCTATTAC			4347
TGCTAAAAAA AAAAAAAAAA			4367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Ser Ala Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu			
1	5	10	15
Ser Arg Arg Phe Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln			
20	25	30	
Arg Pro Ala Arg Arg Ser Gly Arg Gly Gly Gly Gly Ala Ala Pro Gly			
35	40	45	

Pro Tyr Pro Ser Ala Ala Pro Pro Pro Pro Gly Pro Gly Pro Pro Pro
 50 55 60
 Ser Arg Gln Ser Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn
 65 70 75 80
 Gly Asn Gly Gly Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly
 85 90 95
 Leu Gly Gly Pro Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala
 100 105 110
 Ser Pro Gly Ala Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly
 115 120 125
 Ala Arg Ala Ser Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Ala
 130 135 140
 Pro Gly Cys Pro Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr
 145 150 155 160
 Met Ser Leu Lys Pro Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 165 170 175
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Ala
 180 185 190
 Ala Ala Asn Val Arg Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro
 195 200 205
 Ala Ala Ala Pro Ser Pro Ser Ser Ser Ser Val Ser Ser Ser Ser Ala
 210 215 220
 Thr Ala Pro Ser Ser Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro
 225 230 235 240
 Gly Leu Gly Arg Gly Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr
 245 250 255
 Ile Ser Phe Asp Gly Ile Tyr Ala Asn Met Arg Met Val His Ile Leu
 260 265 270
 Thr Ser Val Val Gly Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly
 275 280 285
 Ile Tyr Glu Gly Val Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val
 290 295 300
 Leu Asp Ala Ala His Glu Lys Ser Thr Glu Ser Ser Ser Gly Pro Lys
 305 310 315 320
 Arg Glu Glu Ile Met Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val
 325 330 335
 Val Val Gln Phe Lys Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala
 340 345 350
 Phe Thr Asp Ser Ala Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu
 355 360 365
 Lys Asp Leu Glu Pro Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu

370					375					380					
Leu	Glu	Ala	Leu	Glu	Asn	Asp	Val	Ser	Asn	Gly	Trp	Asp	Pro	Asn	Asp
385					390					395					400
Met	Phe	Arg	Tyr	Asn	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp
				405					410					415	
Ser	Ser	Leu	Ser	Ser	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu
			420					425					430		
Glu	Phe	Leu	Lys	Arg	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile
			435				440						445		
Glu	Ser	Ser	Ala	Gln	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp
			450			455					460				
Arg	Ser	Glu	Glu	Glu	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Ser	Ser	Glu
465					470					475					480
Arg	Glu	Gly	His	Ser	Ile	Asn	Thr	Arg	Glu	Asn	Lys	Tyr	Ile	Pro	Pro
			485						490					495	
Gly	Gln	Arg	Asn	Arg	Glu	Val	Ile	Ser	Trp	Gly	Ser	Gly	Arg	Gln	Asn
			500					505					510		
Ser	Pro	Arg	Met	Gly	Gln	Pro	Gly	Ser	Gly	Ser	Met	Pro	Ser	Arg	Ser
			515				520					525			
Thr	Ser	His	Thr	Ser	Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg
			530			535					540				
Val	Val	Asn	Gly	Gly	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser
545					550					555					560
Ser	Arg	Pro	Pro	Ser	Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro	Pro
				565					570					575	
Arg	Ala	Ala	Thr	Pro	Thr	Arg	Pro	Pro	Ser	Arg	Pro	Pro	Ser	Arg	Pro
			580					585					590		
Ser	Arg	Pro	Pro	Ser	His	Pro	Ser	Ala	His	Gly	Ser	Pro	Ala	Pro	Val
			595				600					605			
Ser	Thr	Met	Pro	Lys	Arg	Met	Ser	Ser	Glu	Gly	Pro	Pro	Arg	Met	Ser
			610			615					620				
Pro	Lys	Ala	Gln	Arg	His	Pro	Arg	Asn	His	Arg	Val	Ser	Ala	Gly	Arg
625					630					635					640
Gly	Ser	Ile	Ser	Ser	Gly	Leu	Glu	Phe	Val	Ser	His	Asn	Pro	Pro	Ser
				645					650					655	
Glu	Ala	Ala	Thr	Pro	Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr
			660					665					670		
Trp	Ser	Ser	Val	Val	Ser	Gly	Val	Pro	Arg	Leu	Ser	Pro	Lys	Thr	His
			675				680					685			
Arg	Pro	Arg	Ser	Pro	Arg	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Pro	Ser	Gly
			690			695					700				

Pro Val Leu Ala Ser Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val
 705 710 715 720
 Ala Met Pro Ile Pro Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser
 725 730 735
 Asn Arg Ala Val Thr Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln
 740 745 750
 Asp Gln Arg Gln Asn Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro
 755 760 765
 Asn Glu Thr Ser Pro Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser
 770 775 780
 Pro Val Val Ser Glu His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe
 785 790 795 800
 Lys Asn Asp Phe Arg Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp
 805 810 815
 Gln Leu Leu Asn Lys Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile
 820 825 830
 Lys Asp Lys Ile Glu Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser
 835 840 845
 Ser Ser Asn Cys Thr Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile
 850 855 860
 Ser Pro Ser Ile Leu Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val
 865 870 875 880
 Thr Ser Gln Gly Val Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys
 885 890 895
 Asp Asp Lys Glu Glu Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser
 900 905 910
 Thr Leu Asn Pro Asn Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln
 915 920 925
 Pro Lys Pro Ser Thr Thr Pro Thr Ser Pro Arg Pro Gln Ala Gln Pro
 930 935 940
 Ser Pro Ser Met Val Gly His Gln Gln Pro Thr Pro Val Tyr Thr Gln
 945 950 955 960
 Pro Val Cys Phe Ala Pro Asn Met Met Tyr Pro Val Pro Val Ser Pro
 965 970 975
 Gly Val Gln Pro Leu Tyr Pro Ile Pro Met Thr Pro Met Pro Val Asn
 980 985 990
 Gln Ala Lys Thr Tyr Arg Ala Val Pro Asn Met Pro Gln Gln Arg Gln
 995 1000 1005
 Asp Gln His His Gln Ser Ala Met Met His Pro Ala Ser Ala Ala Gly
 1010 1015 1020

Pro Pro Ile Ala Ala Thr Pro Pro Ala Tyr Ser Thr Gln Tyr Val Ala
 1025 1030 1035 1040
 Tyr Ser Pro Gln Gln Phe Pro Asn Gln Pro Leu Val Gln His Val Pro
 1045 1050 1055
 His Tyr Gln Ser Gln His Pro His Val Tyr Ser Pro Val Ile Gln Gly
 1060 1065 1070
 Asn Ala Arg Met Met Ala Pro Pro Thr His Ala Gln Pro Gly Leu Val
 1075 1080 1085
 Ser Ser Ser Ala Thr Gln Tyr Gly Ala His Glu Gln Thr His Ala Met
 1090 1095 1100
 Tyr Ala Cys Pro Lys Leu Pro Tyr Asn Lys Glu Thr Ser Pro Ser Phe
 1105 1110 1115 1120
 Tyr Phe Ala Ile Ser Thr Gly Ser Leu Ala Gln Gln Tyr Ala His Pro
 1125 1130 1135
 Asn Ala Thr Leu His Pro His Thr Pro His Pro Gln Pro Ser Ala Thr
 1140 1145 1150
 Pro Thr Gly Gln Gln Gln Ser Gln His Gly Gly Ser His Pro Ala Pro
 1155 1160 1165
 Ser Pro Val Gln His His Gln His Gln Ala Ala Gln Ala Leu His Leu
 1170 1175 1180
 Ala Ser Pro Gln Gln Gln Ser Ala Ile Tyr His Ala Gly Leu Ala Pro
 1185 1190 1195 1200
 Thr Pro Pro Ser Met Thr Pro Ala Ser Asn Thr Gln Ser Pro Gln Asn
 1205 1210 1215
 Ser Phe Pro Ala Ala Gln Gln Thr Val Phe Thr Ile His Pro Ser His
 1220 1225 1230
 Val Gln Pro Ala Tyr Thr Asn Pro Pro His Met Ala His Val Pro Gln
 1235 1240 1245
 Ala His Val Gln Ser Gly Met Val Pro Ser His Pro Thr Ala His Ala
 1250 1255 1260
 Pro Met Met Leu Met Thr Thr Gln Pro Pro Gly Gly Pro Gln Ala Ala
 1265 1270 1275 1280
 Leu Ala Gln Ser Ala Leu Gln Pro Ile Pro Val Ser Thr Thr Ala His
 1285 1290 1295
 Phe Pro Tyr Met Thr His Pro Ser Val Gln Ala His His Gln Gln Gln
 1300 1305 1310
 Leu

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACCACCAGC AACAGCAACA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG	60
CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG	120
CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG	180
CAGCATCAGC GAAACTCTGG GCC	203

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CACCACCAGC AACAGCAACA	20
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(2) INFORMATION FOR SEQ ID NO:5:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCCCAGAGT TTCCGTGATG	20
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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG	60
CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG	120
CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAG	165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCTCACCAT GTCGCTGAAG C	21
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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGACGCTAGA AGGCCGCTG	19
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTGCGGACA TTGGCAGCC

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTCTCAGC CAAAGCCTTC TACTACC

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCGCAGC TCCGCTCCC

19

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCCGGGCCG AAACGCGCCG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCGGTGTC GCGGCGACTT CC

22